

**What we claim is:**

1. A method for increasing the probability of vegetative reproduction of a new plant generation comprising transgenically expressing a gene encoding a protein acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase (SERK).
2. A method according to claim 1, wherein the encoded protein physically interacts with SERK.
3. The method according to claim 2, wherein the protein is a member of the family of Squamosa-promoter Binding Protein (SBP) transcription factors or 14-3-3 type lambda proteins.
4. The method according to claim 2, wherein the protein has the amino acid sequence given in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16, or an amino acid sequence having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% identity with SEQ ID NO: 12 or SEQ ID NO: 16.
5. The method according to claim 1 increasing the probability of vegetative reproduction through seeds (apomixis).
6. The method according to claim 5, wherein the seeds result from non-gametophytic apomixis.
7. The method according to claim 5, wherein the encoded protein is transgenically expressed in the vicinity of the embryo sac.
8. The method according to claim 1 increasing the probability of *in vitro* somatic embryogenesis.

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D3 / The method according to claim 1, wherein expression of the gene is under control of the SERK gene promoter, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis*

AtChitIV gene promoter, The *Arabidopsis* LTP-1 gene promoter, The *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter or the promoter of the O126 gene of *Phalaenopsis*.

10. A gene encoding a protein having the amino acid sequence given in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, or SEQ ID NO: 16, or an amino acid sequence having a component sequence of at least 150 amino acids length which after alignment reveals at least 40% sequence identity with SEQ ID NO: 12 or SEQ ID NO: 16.
11. A gene according to claim 10 having the nucleotide sequence given in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, or SEQ ID NO: 15.
12. A gene according to claim 10 wherein the nucleotide sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the DNA is to be inserted are used.
13. A plant or plant cell transgenically expressing the gene according to any one of claims 10-12.
14. A plant or plant cell obtainable by the method of claim 1.

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